IN THE CLAIMS

Please amend the claims as follows:

Claim 1 (Original): Isolated nucleic acid sequence coding for a polypeptide having acetohydroxy acid synthetase (AHAS) activity selected from the group consisting of:

a) a nucleic acid sequence according to SEQ. ID No: 1 or SEQ. ID NO: 3;

b) a nucleic acid sequence comprising in position 21 and 22 a base triplet coding for Asp and Phe, respectively;

c) a nucleic acid sequence hybridising under stringent conditions with those of a) or b);

d) a nucleic acid sequence having a homology of at least 70% with those of a) or b);

e) a nucleic acid coding for a polypeptide having at least 80% homology on amino acid level with the polypeptide coded by a) or b);

f) a nucleic acid coding for a polypeptide with improved activity and/or selectivity and/or stability as compared with the polypeptide coded by a) or b), prepared by

i) mutagenesis of a nucleic acid of a) or b),

ii) ligating the nucleic acid sequence obtainable from i) into a suitable vector followed by transformation into a suitable expression system and

iii) expression and detection of the critical polypeptide with improved activity and/or selectivity and/or stability;

g) polynucleotide containing at least 15 successive bases of the polynucleotide sequences of a) - f).

Claim 2 (Original): A polypeptide selected from the group consisting of:

a) a polypeptide coded by a nucleic acid sequence according to Claim 1;

b) a polypeptide having a sequence in accordance with SEQ. ID NO: 2 or SEQ. ID NO: 4;

c) a polypeptide which is at least 84% homologous to a polypeptide with SEQ. ID NO: 2 or SEQ: ID NO. 4, without the activity and/or selectivity and/or stability of the polypeptide being substantially reduced as compared with the polypeptide with SEQ. ID NO: 2 or SEQ. ID NO: 4.

Claim 3 (Currently Amended): Plasmids, vectors, micro-organisms comprising one or more nucleic acid sequences according to ~~Claims~~ Claim1.

Claim 4 (Original): Primers for preparing - by means of PCR - or hybridisation probes for detecting the nucleic acid sequences according to Claim 1.

Claim 5 (Original): A process for preparing improved rec-polypeptides with acetohydroxy acid synthetase (AHAS) activity starting from nucleic acid sequences in accordance with Claim 1,

characterised in that

a) the nucleic acid sequences are subjected to mutagenesis,

b) the nucleic acid sequences obtainable from a) are cloned in a suitable vector and these are transferred into a suitable expression system and

c) the polypeptides with improved activity and/or selectivity and/or stability which are formed are detected and isolated.

Claim 6 (Original): rec-polypeptides or nucleic acid sequences coding for these, obtainable in accordance with Claim 5.

Claim 7 (Currently Amended): The use of the polypeptides in accordance with Claim 2 ~~or 6~~ to prepare enantiomer-enriched branched-chain amino acids.

Claim 8 (Currently Amended): Use of the nucleic acid sequences in accordance with Claim 1 ~~or 6~~ to prepare an amino acid producing micro-organism.

Claim 9 (Original): Process for the production of a branched-chain amino acid using a polypeptide of Claim 2.

Claim 10 (Original): Vector pECKA or pECKA/ilvBNC.

Claim 11 (Original): Micro-organisms: DSM15652, DSM15651, DSM15650.